

SEQUENCE LISTING

<110> Sprecher, Cindy A.
 Presnell, Scott R.
 Gao, Zeren
 Whitmore, Theodore E.
 Kuijper, Joseph L.
 Maurer, Mark F.

<120> CYTOKINE RECEPTOR ZCYTOR17

<130> 00-42

<150> US 60/214,282

<151> 2000-06-26

<150> US 60/214,955

<151> 2000-06-29

<150> US 60/267,963

<151> 2001-08-02

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<213> Homo sapiens

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aatgtccgca aaacattctc tctccccagc cttcatgtgt taacctgggg atg atg	176
Met Met	

tgg acc tgg gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu 5 10 15	224
gca gct ctg cca gct aag cct gag aac att tcc tgt gtc tac tac tat Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr 20 25 30	272
agg aaa aat tta acc tgc act tgg agt cca gga aag gaa acc agt tat Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr 35 40 45 50	320
acc cag tac aca gtt aag aga act tac gct ttt gga gaa aaa cat gat Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp 55 60 65	368
aat tgt aca acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser 70 75 80	416
ttt ttc ctt cca aga ata acg atc cca gat aat tat acc att gag gtg Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val 85 90 95	464
gaa gct gaa aat gga gat ggt gta att aaa tct cat atg aca tac tgg Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp 100 105 110	512
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aaa cca gtt ttg ggc atc aaa cga atg att caa att gaa tgg ata aag Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys 135 140 145	608
cct gag ttg gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe 150 155 160	656
agg aca gtc aac agt acc agc tgg atg gaa gtc aac ttc gct aag aac Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn 165 170 175	704

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cgt Arg	aag Lys	gat Asp	aaa Lys	aac Asn	caa Gln	acg Thr	tac Tyr	aac Asn	ctc Leu	acg Thr	ggg Gly	ctg Leu	cag Gln	cct Pro	ttt Phe	752
180						185			190							
aca Thr	gaa Glu	tat Tyr	gtc Val	ata Ile	gct Ala	ctg Leu	cga Arg	tgt Cys	gcg Ala	gtc Val	aag Lys	gag Glu	tca Ser	aag Lys	ttc Phe	800
195			200						205			210				
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			215						220			225				
cca Pro	tgt Cys	ggc Gly	ctg Leu	gaa Glu	ctg Leu	tgg Trp	aga Arg	gtc Val	ctg Leu	aaa Lys	cca Pro	gct Ala	gag Glu	gcg Ala	gat Asp	896
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gga Gly	aga Arg	agg Arg	cca Pro	gtg Val	cgg Arg	ttg Leu	tta Leu	tgg Trp	aag Lys	aag Lys	gca Ala	aga Arg	gga Gly	gcc Ala	cca Pro	944
245						250						255				
gtc Val	cta Leu	gag Glu	aaa Lys	aca Thr	ctt Leu	ggc Gly	tac Tyr	aac Asn	ata Ile	tgg Trp	tac Tyr	tat Tyr	cca Pro	gaa Glu	agc Ser	992
260						265						270				
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275			280						285			290				
ctg Leu	cat His	ctg Leu	gga Gly	ggc Gly	gag Glu	agc Ser	ttt Phe	tgg Trp	gtg Val	tct Ser	atg Met	att Ile	tct Ser	tat Tyr	aat Asn	1088
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tct Ser	ctt Leu	ggg Gly	aag Lys	tct Ser	cca Pro	gtg Val	gcc Ala	acc Thr	ctg Leu	agg Arg	att Ile	cca Pro	gct Ala	att Ile	caa Gln	1136
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Asp	Gln	Leu	Val	Val	Lys	Trp	Gln	Ser	Ser	Ala	Leu	Asp	Val	Asn	Thr	
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Trp	Met	Ile	Glu	Trp	Phe	Pro	Asp	Val	Asp	Ser	Glu	Pro	Thr	Thr	Leu	
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tcc	tgg	gaa	tct	gtg	tct	cag	gcc	acg	aac	tgg	acg	atc	cag	caa	gat	1328
Ser	Trp	Glu	Ser	Val	Ser	Gln	Ala	Thr	Asn	Trp	Thr	Ile	Gln	Gln	Asp	
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aaa	tta	aaa	cct	ttc	tgg	tgc	tat	aac	atc	tct	gtg	tat	cca	atg	ttg	1376
Lys	Leu	Lys	Pro	Phe	Trp	Cys	Tyr	Asn	Ile	Ser	Val	Tyr	Pro	Met	Leu	
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His	Asp	Lys	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	Ala	Lys	Glu	
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Gly	Val	Pro	Ser	Glu	Gly	Pro	Glu	Thr	Lys	Val	Glu	Asn	Ile	Gly	Val	
	420					425					430					
aag	acg	gtc	acg	atc	aca	tgg	aaa	gag	att	ccc	aag	agt	gag	aga	aag	1520
Lys	Thr	Val	Thr	Ile	Thr	Trp	Lys	Glu	Ile	Pro	Lys	Ser	Glu	Arg	Lys	
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ggc	atc	atc	tgc	aac	tac	acc	atc	ttt	tac	caa	gct	gaa	ggc	gga	aaa	1568
Gly	Ile	Ile	Cys	Asn	Tyr	Thr	Ile	Phe	Tyr	Gln	Ala	Glu	Gly	Gly	Lys	
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gga	ttc	tcc	aag	aca	gtc	aat	tcc	agc	atc	ttg	cag	tac	ggc	ctg	gag	1616
Gly	Phe	Ser	Lys	Thr	Val	Asn	Ser	Ser	Ile	Leu	Gln	Tyr	Gly	Leu	Glu	
			470					475					480			
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Ser	Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	Ala	Ser	Thr	
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ctt	ctt	att	ctc	att	atc	ctg	aca	gtg	gca	tat	ggt	ctc	aaa	aaa	ccc	1808
Leu	Leu	Ile	Leu	Ile	Ile	Leu	Thr	Val	Ala	Tyr	Gly	Leu	Lys	Lys	Pro	
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aac	aaa	ttg	act	cat	ctg	tgt	tgg	ccc	acc	gtt	ccc	aac	cct	gct	gaa	1856
Asn	Lys	Leu	Thr	His	Leu	Cys	Trp	Pro	Thr	Val	Pro	Asn	Pro	Ala	Glu	
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Leu	Lys	Glu	Ser	Asp	Asp	Ser	Val	Asn	Thr	Glu	Asp	Arg	Ile	Leu	Lys	
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Gly	Gln	Glu	Asn	Asn	Leu	Gly	Gly	Glu	Lys	Asn	Gly	Tyr	Val	Thr	Cys	
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Pro	Phe	Arg	Pro	Asp	Cys	Pro	Leu	Gly	Lys	Ser	Phe	Glu	Glu	Leu	Pro	
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Val	Ser	Pro	Glu	Ile	Pro	Pro	Arg	Lys	Ser	Gln	Tyr	Leu	Arg	Ser	Arg	
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Met Pro Glu Gly Thr Arg Pro Glu Ala Lys Glu Gln Leu Leu Phe Ser
675 680 685 690

ggt caa agt tta gta cca gat cat ctg tgt gag gaa gga gcc cca aat 2288
Gly Gln Ser Leu Val Pro Asp His Leu Cys Glu Glu Gly Ala Pro Asn
695 700 705

cca tat ttg aaa aat tca gtg aca gcc agg gaa ttt ctt gtg tct gaa 2336
Pro Tyr Leu Lys Asn Ser Val Thr Ala Arg Glu Phe Leu Val Ser Glu
710 715 720

aaa ctt cca gag cac acc aag gga gaa gtc taaatgcgac catagcatga 2386
Lys Leu Pro Glu His Thr Lys Gly Glu Val
725 730

gaccctcggg gcctca 2402

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35 40 45
Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
50 55 60
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
65 70 75 80
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
85 90 95
Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
100 105 110
Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
115 120 125
Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
130 135 140

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Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
 145 150 155 160
 Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
 165 170 175
 Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
 180 185 190
 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
 195 200 205
 Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
 210 215 220
 Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu
 225 230 235 240
 Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly
 245 250 255
 Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro
 260 265 270
 Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln
 275 280 285
 Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser
 290 295 300
 Tyr Asn Ser Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala
 305 310 315 320
 Ile Gln Glu Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val
 325 330 335
 Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val
 340 345 350
 Asn Thr Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr
 355 360 365
 Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln
 370 375 380
 Gln Asp Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro
 385 390 395 400
 Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala
 405 410 415
 Lys Glu Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile
 420 425 430
 Gly Val Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu
 435 440 445
 Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly
 450 455 460
 Gly Lys Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly
 465 470 475 480

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Leu Glu Ser Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala
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 Ser Thr Ser Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr
 500 505 510
 Leu Ser Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly
 515 520 525
 Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys
 530 535 540
 Lys Pro Asn Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro
 545 550 555 560
 Ala Glu Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys
 565 570 575
 Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile
 580 585 590
 Leu Lys Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu
 595 600 605
 Val Val Asn Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala
 610 615 620
 Arg Thr Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Tyr Val
 625 630 635 640
 Thr Cys Pro Phe Arg Pro Asp Cys Pro Leu Gly Lys Ser Phe Glu Glu
 645 650 655
 Leu Pro Val Ser Pro Glu Ile Pro Pro Arg Lys Ser Gln Tyr Leu Arg
 660 665 670
 Ser Arg Met Pro Glu Gly Thr Arg Pro Glu Ala Lys Glu Gln Leu Leu
 675 680 685
 Phe Ser Gly Gln Ser Leu Val Pro Asp His Leu Cys Glu Glu Gly Ala
 690 695 700
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<210> 3

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<223> WSXWS peptide motif

<221> VARIANT

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0902290" 64626860

<223> Xaa = Any Amino Acid

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<210> 4

<211> 2196

<212> DNA

<213> Artificial Sequence

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<221> misc_feature

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<223> n = A,T,C or G

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tgywsnttyt	tyytncnmg	nathacnath	ccngayaayt	ayacnathga	rgtnngargcn	300
garaayggng	ayggngtnat	haarwsncay	atgacntayt	ggmgnytnga	raayathgcn	360
aaracngarc	cncnnaarat	httymgngtn	aarccngtny	tnggnathaa	rmgnatgath	420
carathgart	ggathaarcc	ngarytngcn	ccngtnwsnw	sngayytnaa	rtayacnytn	480
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gayaaraayc	aracntayaa	yytnacnggn	ytncarcnt	tyacngarta	ygtnathgcn	600
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acnatgaaya	cnacnaayca	rcarytngar	ytncayytng	gnggngarws	nttytgggtg	900
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athcargara	arwsnttyca	rtgyathgar	gtnatgcarg	cntgygtngc	ngargaycar	1020
ytngtngtna	artggcarws	nwsngcnyn	gaygtnaaya	cntggatgat	hgartgggtt	1080
ccngaygtng	aywsngarcc	nacnacnytn	wsntgggarw	sngtnwsnca	rgcnacnaay	1140
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cargcngarg	gnggnaargg	nttywsnaar	acngtnaayw	snwsnathyt	ncartayggg	1440

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ccngarathc	cncnmgnaa	rwsncartay	ytnmgnwsnm	gnatgccnga	rggnacnmgn	2040
ccngargcna	argarcaryt	nytnnttywsn	ggncarwsny	tngtnccnga	ycayytntgy	2100
gargarggng	cncnaaycc	ntayytnaar	aaywsngtna	cngcnmgnga	rttyytngtn	2160
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<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC12701

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<210> 6

<211> 23

<212> DNA

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<223> Oligonucleotide primer ZC27898

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<210> 7

<211> 25

<212> DNA

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<223> Oligonucleotide primer ZC14063

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<223> Oligonucleotide primer ZC27899

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ccagaacttt gactccttga ccg 23

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aaaacattct ctctccccag ccttcatgtg ttaacctggg gatgatgtgg acctgggcac 180
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aaaccagtta taccagctac acagttaaga gaacttacgc ttttggagaa aaacatgata 360
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gaataacgat cccagataat tataaccattg aggtggaagc tgaaaatgga gatggtgtaa 480
ttaaattctca tatgacatac tggagattag agaacatagc gaaaactgaa ccacctaaga 540
ttttccgtgt gaaaccagtt ttgggcatca aacgaatgat tcaaattgaa tggataaagc 600
ctgagttggc gcctgtttca tctgatttaa aatacacact tcgattcagg acagtcaaca 660
gtaccagctg gatggaagtc aacttcgcta agaaccgtaa ggataaaaac caaacgtaca 720
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<400> 13
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09892949-062601
T09290-64626860

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aaaacattct ctctccccag ccttcatgtg ttaacctggg g atg atg tgg acc tgg 176
                                         Met Met Trp Thr Trp
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gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg 224
Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu
          10             15             20

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cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat 272
Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn
          25             30             35

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tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac 320
Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr
          40             45             50

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aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca 368
Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr
          55             60             65

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acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct ttt ttc ctt 416

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T09290.6462860

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Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile	Glu	Val	Glu	Ala	Glu	
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Asn	Gly	Asp	Gly	Val	Ile	Lys	Ser	His	Met	Thr	Tyr	Trp	Arg	Leu	Glu	
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Leu	Gly	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp	Ile	Lys	Pro	Glu	Leu	
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Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala	Lys	Asn	Arg	Lys	Asp	
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Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln	Pro	Phe	Thr	Glu	Tyr	
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Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Glu	Ala	Pro	Cys	Gly	
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ctg	gaa	ctg	tgg	aga	gtc	ctg	aaa	cca	gct	gag	gcg	gat	gga	aga	agg	896
Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu	Ala	Asp	Gly	Arg	Arg	
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09992949.062601

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aaa aca ctt ggc tac aac ata tgg tac tat cca gaa agc aac act aac 992
 Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn Thr Asn
 265 270 275

ctc aca gaa aca atg aac act act aac cag cag ctt gaa ctg cat ctg 1040
 Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu His Leu
 280 285 290

gga ggc gag agc ttt tgg gtg tct atg att tct tat aat tct ctt ggg 1088
 Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser Leu Gly
 295 300 305

aag tct cca gtg gcc acc ctg agg att cca gct att caa gaa aaa 1133
 Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu Lys
 310 315 320

tagaaacttt acagatgcta gtcccagaca taaaagaaaa taatgttctg gatgtgcacg 1193
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 35 40 45
 Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
 50 55 60
 His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
 65 70 75 80
 Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
 85 90 95

09892949.062601

Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
 100 105 110
 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
 115 120 125
 Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
 130 135 140
 Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
 145 150 155 160
 Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
 165 170 175
 Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
 180 185 190
 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
 195 200 205
 Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
 210 215 220
 Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu
 225 230 235 240
 Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly
 245 250 255
 Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro
 260 265 270
 Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln
 275 280 285
 Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser
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 aaaacattct ctctccccag ccttcatgtg ttaacctggg g atg atg tgg acc tgg 176
 Met Met Trp Thr Trp
 1 5

gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg 224
 Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu
 10 15 20

cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat 272
 Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn
 25 30 35

tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac 320
 Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr
 40 45 50

aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca 368
 Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr
 55 60 65

acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct ttt ttc ctt 416

09892949.062601

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Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser	Lys	Phe	Trp	Ser	Asp	
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Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Glu	Gly	Lys	Leu	Leu	
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T09290" 64626860

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<213> Homo sapiens

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 35          40          45
Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
 50          55          60
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
 65          70          75          80
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
 85          90          95
Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
100          105          110
Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
115          120          125
Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
130          135          140
Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
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Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
165          170          175
Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
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Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
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09892949.062601

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09892949-062601

<220>

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<210> 27

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<210> 29

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<211> 33

<212> DNA

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<223> Oligonucleotide primer ZC17212

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33

<210> 31

<211> 30

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<400> 31

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T.092290" 64626860

<213> Artificial Sequence

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1 5

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<211> 8

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<213> Artificial Sequence

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1 5

<210> 36

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<212> DNA

0982949 "062601

<213> Homo sapiens

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agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	96
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	
			20					25					30			

ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	144
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	
		35					40					45				

ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	192
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	
	50					55					60					

ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	240
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	
65					70				75					80		

tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	288
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	
			85					90						95		

aaa	gtt	gag	ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	336
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	
			100					105					110			

cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	384
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	
		115				120						125				

aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	432
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	
	130					135					140					

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gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg	480
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp	
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Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu	
165 170 175	
gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg	576
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu	
180 185 190	
cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac	624
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn	
195 200 205	
aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg	672
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly	
210 215 220	
cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag	720
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu	
225 230 235 240	
ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat	768
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr	
245 250 255	
ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac	816
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn	
260 265 270	
aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc	864
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe	
275 280 285	
ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac	912
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn	
290 295 300	
gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg	960
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr	
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 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

990

<210> 38
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 <212> PRT
 <213> Homo sapiens

<400> 38

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			20				25						30		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
		35				40						45			
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
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Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
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Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
			85					90						95	
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
			100					105						110	
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
			115				120						125		
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
	130					135					140				
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp
145					150					155				160	
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
			165					170						175	
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
			180					185					190		
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
		195				200						205			
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
	210					215					220				
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu
225					230					235				240	
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
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Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
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 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
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 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

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<220>
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ttg aaa tct ggt acc gcc tct gtt gtg tgc ctg ctg aat aac ttc tat 96
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 20 25 30

ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg 144
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 35 40 45

ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc 192
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 50 55 60

tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa 240
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 65 70 75 80

cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc 288

09892940 062650

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
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 100 105

321

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 <213> Homo sapiens

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 20 25 30
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 35 40 45
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 50 55 60
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 65 70 75 80
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 85 90 95
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 100 105

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 <223> Oligonucleotide primer ZC11440

<400> 41
 aattgaga

8

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09892949.062601

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<400> 42

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8

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aactgtagat ttctaggaat tcaatccttg gccacgcgctc 100

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<212> DNA

<213> Artificial Sequence

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aaaacattct ctctccccag ccttcatgtg ttaacctggg g atg atg tgg acc tgg	176
Met Met Trp Thr Trp	
1 5	
gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg	224
Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu	
10 15 20	
cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat	272
Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn	
25 30 35	
tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac	320
Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr	
40 45 50	
aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca	368
Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr	
55 60 65	
acc aat agt tct aca agt gaa aat cgt gct tgc tgc tct ttt ttc ctt	416
Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu	
70 75 80 85	
cca aga ata acg atc cca gat aat tat acc att gag gtg gaa gct gaa	464
Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu	
90 95 100	
aat gga gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag	512
Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu	
105 110 115	
aac ata gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt	560
Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val	
120 125 130	
ttg ggc atc aaa cga atg att caa att gaa tgg ata aag cct gag ttg	608
Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu	
135 140 145	
gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc	656

Ala	Pro	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu	Arg	Phe	Arg	Thr	Val		
150					155					160					165		
aac	agt	acc	agc	tgg	atg	gaa	gtc	aac	ttc	gct	aag	aac	cgt	aag	gat	704	
Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala	Lys	Asn	Arg	Lys	Asp		
				170				175					180				
aaa	aac	caa	acg	tac	aac	ctc	acg	ggg	ctg	cag	cct	ttt	aca	gaa	tat	752	
Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln	Pro	Phe	Thr	Glu	Tyr		
			185					190					195				
gtc	ata	gct	ctg	cga	tgt	gcg	gtc	aag	gag	tca	aag	ttc	tgg	agt	gac	800	
Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser	Lys	Phe	Trp	Ser	Asp		
		200					205					210					
tgg	agc	caa	gaa	aaa	atg	gga	atg	act	gag	gaa	gaa	gct	cca	tgt	ggc	848	
Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Glu	Ala	Pro	Cys	Gly		
	215					220					225						
ctg	gaa	ctg	tgg	aga	gtc	ctg	aaa	cca	gct	gag	gcg	gat	gga	aga	agg	896	
Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu	Ala	Asp	Gly	Arg	Arg		
230					235				240				245				
cca	gtg	cgg	ttg	tta	tgg	aag	aag	gca	aga	gga	gcc	cca	gtc	cta	gag	944	
Pro	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val	Leu	Glu		
			250					255					260				
aaa	aca	ctt	ggc	tac	aac	ata	tgg	tac	tat	cca	gaa	agc	aac	act	aac	992	
Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro	Glu	Ser	Asn	Thr	Asn		
		265					270					275					
ctc	aca	gaa	aca	atg	aac	act	act	aac	cag	cag	ctt	gaa	ctg	cat	ctg	1040	
Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln	Leu	Glu	Leu	His	Leu		
		280					285					290					
gga	ggc	gag	agc	ttt	tgg	gtg	tct	atg	att	tct	tat	aat	tct	ctt	ggg	1088	
Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser	Tyr	Asn	Ser	Leu	Gly		
	295					300					305						
aag	tct	cca	gtg	gcc	acc	ctg	agg	att	cca	gct	att	caa	gaa	aaa	tca	1136	
Lys	Ser	Pro	Val	Ala	Thr	Leu	Arg	Ile	Pro	Ala	Ile	Gln	Glu	Lys	Ser		
310					315				320						325		

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Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp Gln Leu	
330 335 340	
gtg gtg aag tgg caa agc tct gct cta gac gtg aac act tgg atg att	1232
Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp Met Ile	
345 350 355	
gaa tgg ttt ccg gat gtg gac tca gag ccc acc acc ctt tcc tgg gaa	1280
Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser Trp Glu	
360 365 370	
tct gtg tct cag gcc acg aac tgg acg atc cag caa gat aaa tta aaa	1328
Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys Leu Lys	
375 380 385	
cct ttc tgg tgc tat aac atc tct gtg tat cca atg ttg cat gac aaa	1376
Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His Asp Lys	
390 395 400 405	
gtt ggc gag cca tat tcc atc cag gct tat gcc aaa gaa ggc gtt cca	1424
Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly Val Pro	
410 415 420	
tca gaa ggt cct gag acc aag gtg gag aac att ggc gtg aag acg gtc	1472
Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys Thr Val	
425 430 435	
acg atc aca tgg aaa gag att ccc aag agt gag aga aag ggt atc atc	1520
Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly Ile Ile	
440 445 450	
tgc aac tac acc atc ttt tac caa gct gaa ggt gga aaa gga ttc tcc	1568
Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly Phe Ser	
455 460 465	
aag aca gtc aat tcc agc atc ttg cag tac ggc ctg gag tcc ctg aaa	1616
Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser Leu Lys	
470 475 480 485	
cga aag acc tct tac att gtt cag gtc atg gcc agc acc agt gct ggg	1664

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Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	Ala	Ser	Thr	Ser	Ala	Gly	
				490					495					500		
gga	acc	aac	ggg	acc	agc	ata	aat	ttc	aag	aca	ttg	tca	ttc	agt	gtc	1712
Gly	Thr	Asn	Gly	Thr	Ser	Ile	Asn	Phe	Lys	Thr	Leu	Ser	Phe	Ser	Val	
			505					510					515			
ttt	gag	att	atc	ctc	ata	act	tct	ctg	att	ggg	gga	ggc	ctt	ctt	att	1760
Phe	Glu	Ile	Ile	Leu	Ile	Thr	Ser	Leu	Ile	Gly	Gly	Gly	Leu	Leu	Ile	
			520					525					530			
ctc	att	atc	ctg	aca	gtg	gca	tat	ggg	ctc	aaa	aaa	ccc	aac	aaa	ttg	1808
Leu	Ile	Ile	Leu	Thr	Val	Ala	Tyr	Gly	Leu	Lys	Lys	Pro	Asn	Lys	Leu	
			535					540				545				
act	cat	ctg	tgt	tgg	ccc	acc	gtt	ccc	aac	cct	gct	gaa	agt	agt	ata	1856
Thr	His	Leu	Cys	Trp	Pro	Thr	Val	Pro	Asn	Pro	Ala	Glu	Ser	Ser	Ile	
550							555			560					565	
gcc	aca	tgg	cat	gga	gat	gat	ttc	aag	gat	aag	cta	aac	ctg	aag	gag	1904
Ala	Thr	Trp	His	Gly	Asp	Asp	Phe	Lys	Asp	Lys	Leu	Asn	Leu	Lys	Glu	
				570					575					580		
tct	gat	gac	tct	gtg	aac	aca	gaa	gac	agg	atc	tta	aaa	cca	tgt	tcc	1952
Ser	Asp	Asp	Ser	Val	Asn	Thr	Glu	Asp	Arg	Ile	Leu	Lys	Pro	Cys	Ser	
			585					590					595			
acc	ccc	agt	gac	aag	ttg	gtg	att	gac	aag	ttg	gtg	gtg	aac	ttt	ggg	2000
Thr	Pro	Ser	Asp	Lys	Leu	Val	Ile	Asp	Lys	Leu	Val	Val	Asn	Phe	Gly	
			600					605				610				
aat	gtt	ctg	caa	gaa	att	ttc	aca	gat	gaa	gcc	aga	acg	ggg	cag	gaa	2048
Asn	Val	Leu	Gln	Glu	Ile	Phe	Thr	Asp	Glu	Ala	Arg	Thr	Gly	Gln	Glu	
			615				620				625					
aac	aat	tta	gga	ggg	gaa	aag	aat	ggg	act	aga	att	ctg	tct	tcc	tgc	2096
Asn	Asn	Leu	Gly	Gly	Glu	Lys	Asn	Gly	Thr	Arg	Ile	Leu	Ser	Ser	Cys	
630						635			640						645	
cca	act	tca	ata	taagtgtgga	ctaaaatg	cg	agaaagg	tgt	cctgtgtgtct							2148
Pro	Thr	Ser	Ile													

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atgcaaatta gaaaggacat gcagagtttt ccaactagga agactgaatc tgtggcccca 2208
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 gcaatctgta atgcatgtgc atgagaagtc tgttattaag tagagtgtga aaacatgggt 2328
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 ataataccat ttatcatgtaa tgctatactt ctatactatt ttcattgtaat actatacttc 2448
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 35 40 45
 Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
 50 55 60
 His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
 65 70 75 80
 Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
 85 90 95
 Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
 100 105 110
 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
 115 120 125
 Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
 130 135 140
 Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
 145 150 155 160
 Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
 165 170 175
 Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
 180 185 190
 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
 195 200 205
 Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
 210 215 220

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Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu
 225 230 235 240
 Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly
 245 250 255
 Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro
 260 265 270
 Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln
 275 280 285
 Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser
 290 295 300
 Tyr Asn Ser Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala
 305 310 315 320
 Ile Gln Glu Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val
 325 330 335
 Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val
 340 345 350
 Asn Thr Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr
 355 360 365
 Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln
 370 375 380
 Gln Asp Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro
 385 390 395 400
 Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala
 405 410 415
 Lys Glu Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile
 420 425 430
 Gly Val Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu
 435 440 445
 Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly
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 Gly Lys Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly
 465 470 475 480
 Leu Glu Ser Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala
 485 490 495
 Ser Thr Ser Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr
 500 505 510
 Leu Ser Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly
 515 520 525
 Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys
 530 535 540
 Lys Pro Asn Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro
 545 550 555 560

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Ala Glu Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys
 565 570 575
 Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile
 580 585 590
 Leu Lys Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu
 595 600 605
 Val Val Asn Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala
 610 615 620
 Arg Thr Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg
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 Ile Leu Ser Ser Cys Pro Thr Ser Ile
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<210> 47

<211> 1947

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence of SEQ ID NO:46

<221> misc_feature

<222> (1)...(1947)

<223> n = A,T,C or G

<400> 47

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acntggwsnc	cnggnaarga	racnwsntay	acncartaya	cngtnaarmg	nacntaygcn	180
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tgywsnttyt	tyytncnmg	nathacnath	ccngayaayt	ayacnathga	rgtnngargcn	300
garaayggng	ayggngtnat	haarwsncay	atgacntayt	ggmgnytnga	raayathgcn	360
aaracngarc	cncnnaarat	httymgngtn	aarccngtny	tnggnathaa	rmgnatgath	420
carathgart	ggathaarcc	ngarytnngcn	ccngtnwsnw	sngayytnaa	rtayacnytn	480
mgnttymgna	cngtnaayws	nacnwsntgg	atggargtna	ayttygcnaa	raaymgnaar	540
gayaaraayc	aracntayaa	yytnacnggn	ytncarccnt	tyacngarta	ygtcnathgcn	600
ytmgntgyg	cngtnaarga	rwsnaartty	tggwsngayt	ggwsncarga	raaratgggn	660
atgacngarg	argargcncc	ntgyggnytn	garytnctggm	gngtnytnaa	rccngcngar	720
gcngayggnm	gnmgncnngt	nmgnytnytn	tggaaraarg	cnmgnggngc	nccngtnytn	780
garaaracny	tnggntayaa	yathtggtay	tayccngarw	snaayacnaa	yytnacngar	840
acnatgaaya	cnacnaayca	rcarytngar	ytncayytn	gnggngarws	nttytggtgn	900
wsnatgathw	sntayaayws	nytnngnaar	wsnccngtn	cnacnytnmg	nathccngcn	960

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athcargara arwsnttyca rtgyathgar gtnatgcarg cntgygtngc ngargaycar 1020
 ytngtngtna artggcarws nwsngcnytn gaygtnaaya cntggatgat hgartggtty 1080
 ccngaygtng aywsngarcc nacnacnytn wsntgggarw sngtnwsnca rgcnacnaay 1140
 tggacnathc arcargayaa rythnaarccn ttytggtgyt ayaayathws ngntayccn 1200
 atgytncaayg ayaargtngg ngarccntay wsnathcarg cntaygcnaa rgarggngtn 1260
 ccnwsngarg gncngarac naargtngar aayathggng tnaaracngt nacnathacn 1320
 tggaargara thccnaarws ngarmgnaar ggnathatht gyaaytayac nathttytay 1380
 cargcngarg gnggnaargg nttywsnaar acngtnaayw snwsnathyt ncartayggn 1440
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 ggnggnacna ayggnacnws nathaaytty aaracnytnw snttywsngt nttygarath 1560
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 gcngarwsnw snathgcnac ntggcayggn gaygayttya argayaaryt naayytnaar 1740
 garwsngayg aywsngtnaa yacngargay mgnathytna arccntgyws nacnccnwsn 1800
 gayaarytng tnathgayaa rytngtngtn aayttyggna aygtnytnca rgarathtty 1860
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<210> 48

<211> 32

<212> PRT

<213> Homo sapiens

<400> 48

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			20					25					30		

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<211> 23

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<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC21195

<400> 49

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<213> Artificial Sequence

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<210> 52

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<212> PRT

<213> Homo sapiens

<400> 52

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5

10

<210> 53

<211> 2903

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (497)...(2482)

<400> 53

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gaatgtccgc	aaaacattag	tttactctt	gtcgccaggt	tggagtacaa	tggcacgac	180
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gtagctggga	ttacagttaa	caataatgca	atccatttcc	cagcataagt	gggtaagtgc	300

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acactcccac	atcttagtgt	ggataaatta	aagtccagat	tggtcttcct	gtcctgactt	420						
gtgctgtggg	aggtggagtt	gcctttgatg	caaatccttt	gagccagcag	aacatctgtg	480						
gaacatcccc	tgatac	atg aag ctc tct ccc	cag cct tca tgt gtt aac	ctg		532						
	Met	Lys	Leu	Ser	Pro	Gln	Pro	Ser	Cys	Val	Asn	Leu
	1				5					10		
ggg atg atg tgg acc tgg gca ctg tgg atg ctc cct tca ctc tgc aaa	580											
Gly Met Met Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys												
15 20 25												
ttc agc ctg gca gct ctg cca gct aag cct gag aac att tcc tgt gtc	628											
Phe Ser Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val												
30 35 40												
tac tac tat agg aaa aat tta acc tgc act tgg agt cca gga aag gaa	676											
Tyr Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu												
45 50 55 60												
acc agt tat acc cag tac aca gtt aag aga act tac gct ttt gga gaa	724											
Thr Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu												
65 70 75												
aaa cat gat aat tgt aca acc aat agt tct aca agt gaa aat cgt gct	772											
Lys His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala												
80 85 90												
tcg tgc tct ttt ttc ctt cca aga ata acg atc cca gat aat tat acc	820											
Ser Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr												
95 100 105												
att gag gtg gaa gct gaa aat gga gat ggt gta att aaa tct cat atg	868											
Ile Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met												
110 115 120												
aca tac tgg aga tta gag aac ata gcg aaa act gaa cca cct aag att	916											
Thr Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile												
125 130 135 140												
ttc cgt gtg aaa cca gtt ttg ggc atc aaa cga atg att caa att gaa	964											
Phe Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu												
145 150 155												

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335 340 345	
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Val Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp	
350 355 360	
gtg aac act tgg atg att gaa tgg ttt ccg gat gtg gac tca gag ccc	1636
Val Asn Thr Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro	
365 370 375 380	
acc acc ctt tcc tgg gaa tct gtg tct cag gcc acg aac tgg acg atc	1684
Thr Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile	
385 390 395	
cag caa gat aaa tta aaa cct ttc tgg tgc tat aac atc tct gtg tat	1732
Gln Gln Asp Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr	
400 405 410	
cca atg ttg cat gac aaa gtt ggc gag cca tat tcc atc cag gct tat	1780
Pro Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr	
415 420 425	
gcc aaa gaa ggc gtt cca tca gaa ggt cct gag acc aag gtg gag aac	1828
Ala Lys Glu Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn	
430 435 440	
att ggc gtg aag acg gtc acg atc aca tgg aaa gag att ccc aag agt	1876
Ile Gly Val Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser	
445 450 455 460	
gag aga aag ggt atc atc tgc aac tac acc atc ttt tac caa gct gaa	1924
Glu Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu	
465 470 475	
ggt gga aaa gga ttc tcc aag aca gtc aat tcc agc atc ttg cag tac	1972
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ggc ctg gag tcc ctg aaa cga aag acc tct tac att gtt cag gtc atg	2020

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Ala	Ser	Thr	Ser	Ala	Gly	Gly	Thr	Asn	Gly	Thr	Ser	Ile	Asn	Phe	Lys	
	510					515				520						
aca	ttg	tca	ttc	agt	gtc	ttt	gag	att	atc	ctc	ata	act	tct	ctg	att	2116
Thr	Leu	Ser	Phe	Ser	Val	Phe	Glu	Ile	Ile	Leu	Ile	Thr	Ser	Leu	Ile	
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ggc	gga	ggc	ctt	ctt	att	ctc	att	atc	ctg	aca	gtg	gca	tat	ggc	ctc	2164
Gly	Gly	Gly	Leu	Leu	Ile	Leu	Ile	Ile	Leu	Thr	Val	Ala	Tyr	Gly	Leu	
				545					550					555		
aaa	aaa	ccc	aac	aaa	ttg	act	cat	ctg	tgt	tgg	ccc	acc	gtt	ccc	aac	2212
Lys	Lys	Pro	Asn	Lys	Leu	Thr	His	Leu	Cys	Trp	Pro	Thr	Val	Pro	Asn	
			560					565					570			
cct	gct	gaa	agt	agt	ata	gcc	aca	tgg	cat	gga	gat	gat	ttc	aag	gat	2260
Pro	Ala	Glu	Ser	Ser	Ile	Ala	Thr	Trp	His	Gly	Asp	Asp	Phe	Lys	Asp	
		575					580					585				
aag	cta	aac	ctg	aag	gag	tct	gat	gac	tct	gtg	aac	aca	gaa	gac	agg	2308
Lys	Leu	Asn	Leu	Lys	Glu	Ser	Asp	Asp	Ser	Val	Asn	Thr	Glu	Asp	Arg	
	590					595					600					
atc	tta	aaa	cca	tgt	tcc	acc	ccc	agt	gac	aag	ttg	gtg	att	gac	aag	2356
Ile	Leu	Lys	Pro	Cys	Ser	Thr	Pro	Ser	Asp	Lys	Leu	Val	Ile	Asp	Lys	
	605				610					615					620	
ttg	gtg	gtg	aac	ttt	ggg	aat	gtt	ctg	caa	gaa	att	ttc	aca	gat	gaa	2404
Leu	Val	Val	Asn	Phe	Gly	Asn	Val	Leu	Gln	Glu	Ile	Phe	Thr	Asp	Glu	
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gcc	aga	acg	ggt	cag	gaa	aac	aat	tta	gga	ggg	gaa	aag	aat	ggg	act	2452
Ala	Arg	Thr	Gly	Gln	Glu	Asn	Asn	Leu	Gly	Gly	Glu	Lys	Asn	Gly	Thr	
			640					645					650			
aga	att	ctg	tct	tcc	tgc	cca	act	tca	ata	taagtgtgga	ctaaaatgcg					2502
Arg	Ile	Leu	Ser	Ser	Cys	Pro	Thr	Ser	Ile							
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gcctttcata caaaaaagcc ataataccat tttcatgtaa tgctatactt ctatactatt 2802
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<211> 662

<212> PRT

<213> Homo sapiens

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      35          40          45
Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
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Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
65          70          75          80
Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe
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Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu
      100          105          110
Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg
      115          120          125
Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys
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Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro
145          150          155          160
Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg
      165          170          175
Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg
      180          185          190
Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr
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Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp
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Arg	Arg	Pro	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val
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Leu	Glu	Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro	Glu	Ser	Asn
		275					280					285			
Thr	Asn	Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln	Leu	Glu	Leu
	290					295					300				
His	Leu	Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser	Tyr	Asn	Ser
305					310					315					320
Leu	Gly	Lys	Ser	Pro	Val	Ala	Thr	Leu	Arg	Ile	Pro	Ala	Ile	Gln	Glu
				325					330					335	
Lys	Ser	Phe	Gln	Cys	Ile	Glu	Val	Met	Gln	Ala	Cys	Val	Ala	Glu	Asp
			340					345					350		
Gln	Leu	Val	Val	Lys	Trp	Gln	Ser	Ser	Ala	Leu	Asp	Val	Asn	Thr	Trp
		355					360					365			
Met	Ile	Glu	Trp	Phe	Pro	Asp	Val	Asp	Ser	Glu	Pro	Thr	Thr	Leu	Ser
	370					375					380				
Trp	Glu	Ser	Val	Ser	Gln	Ala	Thr	Asn	Trp	Thr	Ile	Gln	Gln	Asp	Lys
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Leu	Lys	Pro	Phe	Trp	Cys	Tyr	Asn	Ile	Ser	Val	Tyr	Pro	Met	Leu	His
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Asp	Lys	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	Ala	Lys	Glu	Gly
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Thr	Val	Thr	Ile	Thr	Trp	Lys	Glu	Ile	Pro	Lys	Ser	Glu	Arg	Lys	Gly
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Ile	Ile	Cys	Asn	Tyr	Thr	Ile	Phe	Tyr	Gln	Ala	Glu	Gly	Gly	Lys	Gly
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Phe	Ser	Lys	Thr	Val	Asn	Ser	Ser	Ile	Leu	Gln	Tyr	Gly	Leu	Glu	Ser
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Leu	Ile	Leu	Ile	Ile	Leu	Thr	Val	Ala	Tyr	Gly	Leu	Lys	Lys	Pro	Asn
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Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser
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 Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu
 580 585 590
 Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro
 595 600 605
 Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn
 610 615 620
 Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly
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 <223> n = A,T,C or G

<400> 55

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acnwsntaya	cncartayac	ngtnaarmgn	acntaygcnt	tyggngaraa	rcaygayaay	240
tgyacnacna	aywsnwsnac	nwsngaraay	mgngcnwsnt	gywsnttytt	yytnccnmgn	300
athacnathc	cngayaayta	yacnathgar	gtngargcng	araayggnga	yggngtnath	360
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ttymngntna	arccngtnyt	nggnathaar	mgntatgathc	arathgartg	gathaarccn	480
garytngcnc	cngtnwsnws	ngayytnaar	tayacnytnm	gnntymgnac	ngtnaaywsn	540
acnwsntgga	tggarctnaa	ytytgcnar	aaymgnaarg	ayaaraayca	racntayaay	600
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wsnaarttyt	ggwsngaytg	gwsncargar	aatatgggna	tgacngarga	rgargcnccn	720
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Trp	Ala	Phe	Ser	Phe	Leu	Cys	Lys	Phe	Ser	Leu	Ala	Val	Leu	Pro	Thr		
	35					40					45						
aag	cca	gag	aac	att	tcc	tgc	gtc	ttt	tac	ttc	gac	aga	aat	ctg	act	431	
Lys	Pro	Glu	Asn	Ile	Ser	Cys	Val	Phe	Tyr	Phe	Asp	Arg	Asn	Leu	Thr		
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tgc	act	tgg	aga	cca	gag	aag	gaa	acc	aat	gat	acc	agc	tac	att	gtg	479	
Cys	Thr	Trp	Arg	Pro	Glu	Lys	Glu	Thr	Asn	Asp	Thr	Ser	Tyr	Ile	Val		
				70					75					80			
act	ttg	act	tac	tcc	tat	gga	aaa	agc	aat	tat	agt	gac	aat	gct	aca	527	
Thr	Leu	Thr	Tyr	Ser	Tyr	Gly	Lys	Ser	Asn	Tyr	Ser	Asp	Asn	Ala	Thr		
			85					90					95				
gag	gct	tca	tat	tct	ttt	ccc	cgt	tcc	tgt	gca	atg	ccc	cca	gac	atc	575	
Glu	Ala	Ser	Tyr	Ser	Phe	Pro	Arg	Ser	Cys	Ala	Met	Pro	Pro	Asp	Ile		
	100					105						110					
tgc	agt	gtt	gaa	gta	caa	gct	caa	aat	gga	gat	ggc	aaa	gtt	aaa	tct	623	
Cys	Ser	Val	Glu	Val	Gln	Ala	Gln	Asn	Gly	Asp	Gly	Lys	Val	Lys	Ser		
	115				120				125								
gac	atc	aca	tat	tgg	cat	tta	atc	tcc	ata	gca	aaa	acc	gaa	cca	cct	671	
Asp	Ile	Thr	Tyr	Trp	His	Leu	Ile	Ser	Ile	Ala	Lys	Thr	Glu	Pro	Pro		
	130				135				140					145			
ata	att	tta	agt	gtg	aat	cca	att	tgt	aat	aga	atg	ttc	cag	ata	caa	719	
Ile	Ile	Leu	Ser	Val	Asn	Pro	Ile	Cys	Asn	Arg	Met	Phe	Gln	Ile	Gln		
				150				155					160				
tgg	aaa	ccg	cgt	gaa	aag	act	cgt	ggg	ttt	cct	tta	gta	tgc	atg	ctt	767	
Trp	Lys	Pro	Arg	Glu	Lys	Thr	Arg	Gly	Phe	Pro	Leu	Val	Cys	Met	Leu		
		165					170					175					
cgg	ttc	aga	act	gtc	aac	agt	agc	cgc	tgg	acg	gaa	gtc	aat	ttt	gaa	815	
Arg	Phe	Arg	Thr	Val	Asn	Ser	Ser	Arg	Trp	Thr	Glu	Val	Asn	Phe	Glu		
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tat gtc ctg gct cta cga ttc agg ttc aat gac tca aga tat tgg agc Tyr Val Leu Ala Leu Arg Phe Arg Phe Asn Asp Ser Arg Tyr Trp Ser 210 215 220 225	911
aag tgg agc aaa gaa gaa acc aga gtg act atg gag gaa gtt cca cat Lys Trp Ser Lys Glu Glu Thr Arg Val Thr Met Glu Glu Val Pro His 230 235 240	959
gtc ctg gac ctg tgg aga att ctg gaa cca gca gac atg aac gga gac Val Leu Asp Leu Trp Arg Ile Leu Glu Pro Ala Asp Met Asn Gly Asp 245 250 255	1007
agg aag gtg cga ttg ctg tgg aag aag gca aga gga gcc ccc gtc ttg Arg Lys Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val Leu 260 265 270	1055
gag aaa aca ttt ggc tac cac ata cag tac ttt gca gag aac agc act Glu Lys Thr Phe Gly Tyr His Ile Gln Tyr Phe Ala Glu Asn Ser Thr 275 280 285	1103
aac ctc aca gag ata aac aac atc acc acc cag cag tat gaa ctg ctt Asn Leu Thr Glu Ile Asn Asn Ile Thr Thr Gln Gln Tyr Glu Leu Leu 290 295 300 305	1151
ctg atg agc cag gca cac tct gtg tcc gtg act tct ttt aat tct ctt Leu Met Ser Gln Ala His Ser Val Ser Val Thr Ser Phe Asn Ser Leu 310 315 320	1199
ggc aag tcc caa gag acc atc ctg agg atc cca gat gtc cat gag aag Gly Lys Ser Gln Glu Thr Ile Leu Arg Ile Pro Asp Val His Glu Lys 325 330 335	1247
acc ttc cag tac att aag agc atg cag gcc tac ata gcc gag ccc ctg Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro Leu 340 345 350	1295
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Trp Glu Ser Val Ser Gln Val Thr Asn Trp Thr Ile Glu Gln Asp Lys	
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Leu Lys Pro Phe Thr Cys Tyr Asn Ile Ser Val Tyr Pro Val Leu Gly	
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His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly	
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Thr Pro Leu Lys Gly Pro Glu Thr Arg Val Glu Asn Ile Gly Leu Arg	
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aca gcc acgt atc aca tgg aag gag att cct aag agt gct aggt aat gga	1631
Thr Ala Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Ala Arg Asn Gly	
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Phe Ile Asn Asn Tyr Thr Val Phe Tyr Gln Ala Glu Gly Gly Lys Glu	
470 475 480	
ctc tcc aag act gtt aac tct cat gcc ctgt cag tgt gac ctgt gag tct	1727
Leu Ser Lys Thr Val Asn Ser His Ala Leu Gln Cys Asp Leu Glu Ser	
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Leu Thr Arg Arg Thr Ser Tyr Thr Val Trp Val Met Ala Ser Thr Arg	
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515 520 525	
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Ser Val Phe Glu Ile Val Leu Leu Thr Ser Leu Val Gly Gly Gly Leu
 530 535 540 545

ctt cta ctt agc atc aaa aca gtg act ttt ggc ctc aga aag cca aac 1919
 Leu Leu Leu Ser Ile Lys Thr Val Thr Phe Gly Leu Arg Lys Pro Asn
 550 555 560

cgg ttg act ccc ctg tgt tgt cct gat gtt ccc aac cct gct gaa agt 1967
 Arg Leu Thr Pro Leu Cys Cys Pro Asp Val Pro Asn Pro Ala Glu Ser
 565 570 575

agt tta gcc aca tgg ctc gga gat ggt ttc aag aag tca aat atg aag 2015
 Ser Leu Ala Thr Trp Leu Gly Asp Gly Phe Lys Lys Ser Asn Met Lys
 580 585 590

gag act gga aac tct ggg aac aca gaa gac gtg gtc cta aaa cca tgt 2063
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 595 600 605

ccc gtc ccc gcg gat ctc att gac aag ctg gta gtg aac ttt gag aat 2111
 Pro Val Pro Ala Asp Leu Ile Asp Lys Leu Val Val Asn Phe Glu Asn
 610 615 620 625

ttt ctg gaa gta gtt ttg aca gag gaa gct gga aag ggt cag gcg agc 2159
 Phe Leu Glu Val Val Leu Thr Glu Glu Ala Gly Lys Gly Gln Ala Ser
 630 635 640

att ttg gga gga gaa gcg aat gag tat atc tta tcc cag gaa cca agc 2207
 Ile Leu Gly Gly Glu Ala Asn Glu Tyr Ile Leu Ser Gln Glu Pro Ser
 645 650 655

tgt cct ggc cat tgc tgaagctacc ctgagggtcc aggacagctg tcttggtggc 2262
 Cys Pro Gly His Cys
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Leu	Trp	Ala	Phe	Ser	Phe	Leu	Cys	Lys	Phe	Ser	Leu	Ala	Val	Leu	Pro	35	40	45	
Thr	Lys	Pro	Glu	Asn	Ile	Ser	Cys	Val	Phe	Tyr	Phe	Asp	Arg	Asn	Leu	50	55	60	
Thr	Cys	Thr	Trp	Arg	Pro	Glu	Lys	Glu	Thr	Asn	Asp	Thr	Ser	Tyr	Ile	65	70	75	80
Val	Thr	Leu	Thr	Tyr	Ser	Tyr	Gly	Lys	Ser	Asn	Tyr	Ser	Asp	Asn	Ala	85	90	95	
Thr	Glu	Ala	Ser	Tyr	Ser	Phe	Pro	Arg	Ser	Cys	Ala	Met	Pro	Pro	Asp	100	105	110	
Ile	Cys	Ser	Val	Glu	Val	Gln	Ala	Gln	Asn	Gly	Asp	Gly	Lys	Val	Lys	115	120	125	
Ser	Asp	Ile	Thr	Tyr	Trp	His	Leu	Ile	Ser	Ile	Ala	Lys	Thr	Glu	Pro	130	135	140	
Pro	Ile	Ile	Leu	Ser	Val	Asn	Pro	Ile	Cys	Asn	Arg	Met	Phe	Gln	Ile	145	150	155	160
Gln	Trp	Lys	Pro	Arg	Glu	Lys	Thr	Arg	Gly	Phe	Pro	Leu	Val	Cys	Met	165	170	175	
Leu	Arg	Phe	Arg	Thr	Val	Asn	Ser	Ser	Arg	Trp	Thr	Glu	Val	Asn	Phe	180	185	190	
Glu	Asn	Cys	Lys	Gln	Val	Cys	Asn	Leu	Thr	Gly	Leu	Gln	Ala	Phe	Thr	195	200	205	
Glu	Tyr	Val	Leu	Ala	Leu	Arg	Phe	Arg	Phe	Asn	Asp	Ser	Arg	Tyr	Trp	210	215	220	
Ser	Lys	Trp	Ser	Lys	Glu	Glu	Thr	Arg	Val	Thr	Met	Glu	Glu	Val	Pro	225	230	235	240
His	Val	Leu	Asp	Leu	Trp	Arg	Ile	Leu	Glu	Pro	Ala	Asp	Met	Asn	Gly	245	250	255	
Asp	Arg	Lys	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val	260	265	270	

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Leu	Glu	Lys	Thr	Phe	Gly	Tyr	His	Ile	Gln	Tyr	Phe	Ala	Glu	Asn	Ser	
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Thr	Asn	Leu	Thr	Glu	Ile	Asn	Asn	Ile	Thr	Thr	Gln	Gln	Tyr	Glu	Leu	
		290					295				300					
Leu	Leu	Met	Ser	Gln	Ala	His	Ser	Val	Ser	Val	Thr	Ser	Phe	Asn	Ser	
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Leu	Gly	Lys	Ser	Gln	Glu	Thr	Ile	Leu	Arg	Ile	Pro	Asp	Val	His	Glu	
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Lys	Thr	Phe	Gln	Tyr	Ile	Lys	Ser	Met	Gln	Ala	Tyr	Ile	Ala	Glu	Pro	
			340					345					350			
Leu	Leu	Val	Val	Asn	Trp	Gln	Ser	Ser	Ile	Pro	Ala	Val	Asp	Thr	Trp	
		355					360					365				
Ile	Val	Glu	Trp	Leu	Pro	Glu	Ala	Ala	Met	Ser	Lys	Phe	Pro	Ala	Leu	
		370				375					380					
Ser	Trp	Glu	Ser	Val	Ser	Gln	Val	Thr	Asn	Trp	Thr	Ile	Glu	Gln	Asp	
385					390					395					400	
Lys	Leu	Lys	Pro	Phe	Thr	Cys	Tyr	Asn	Ile	Ser	Val	Tyr	Pro	Val	Leu	
				405					410					415		
Gly	His	Arg	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	Ala	Lys	Glu	
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Gly	Thr	Pro	Leu	Lys	Gly	Pro	Glu	Thr	Arg	Val	Glu	Asn	Ile	Gly	Leu	
		435					440					445				
Arg	Thr	Ala	Thr	Ile	Thr	Trp	Lys	Glu	Ile	Pro	Lys	Ser	Ala	Arg	Asn	
		450				455					460					
Gly	Phe	Ile	Asn	Asn	Tyr	Thr	Val	Phe	Tyr	Gln	Ala	Glu	Gly	Gly	Lys	
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Glu	Leu	Ser	Lys	Thr	Val	Asn	Ser	His	Ala	Leu	Gln	Cys	Asp	Leu	Glu	
				485					490					495		
Ser	Leu	Thr	Arg	Arg	Thr	Ser	Tyr	Thr	Val	Trp	Val	Met	Ala	Ser	Thr	
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Arg	Ala	Gly	Gly	Thr	Asn	Gly	Val	Arg	Ile	Asn	Phe	Lys	Thr	Leu	Ser	
		515					520					525				
Ile	Ser	Val	Phe	Glu	Ile	Val	Leu	Leu	Thr	Ser	Leu	Val	Gly	Gly	Gly	
		530				535					540					
Leu	Leu	Leu	Leu	Ser	Ile	Lys	Thr	Val	Thr	Phe	Gly	Leu	Arg	Lys	Pro	
545					550					555					560	
Asn	Arg	Leu	Thr	Pro	Leu	Cys	Cys	Pro	Asp	Val	Pro	Asn	Pro	Ala	Glu	
				565					570					575		
Ser	Ser	Leu	Ala	Thr	Trp	Leu	Gly	Asp	Gly	Phe	Lys	Lys	Ser	Asn	Met	
			580					585					590			
Lys	Glu	Thr	Gly	Asn	Ser	Gly	Asn	Thr	Glu	Asp	Val	Val	Leu	Lys	Pro	
			595				600					605				

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Cys Pro Val Pro Ala Asp Leu Ile Asp Lys Leu Val Val Asn Phe Glu
 610 615 620
 Asn Phe Leu Glu Val Val Leu Thr Glu Glu Ala Gly Lys Gly Gln Ala
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<210> 66
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<221> CDS

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Met	Lys	Leu	Ser	Pro	Gln	Pro	Ser	Cys	Val	Asn	Leu	Gly	Met	Met	Trp	
1				5					10						15	

acc	tgg	gca	ctg	tgg	atg	ctc	cct	tca	ctc	tgc	aaa	ttc	agc	ctg	gca	96
Thr	Trp	Ala	Leu	Trp	Met	Leu	Pro	Ser	Leu	Cys	Lys	Phe	Ser	Leu	Ala	
			20					25					30			

gct	ctg	cca	gct	aag	cct	gag	aac	att	tcc	tgt	gtc	tac	tac	tat	agg	144
Ala	Leu	Pro	Ala	Lys	Pro	Glu	Asn	Ile	Ser	Cys	Val	Tyr	Tyr	Tyr	Arg	
		35					40					45				

aaa	aat	tta	acc	tgc	act	tgg	agt	cca	gga	aag	gaa	acc	agt	tat	acc	192
Lys	Asn	Leu	Thr	Cys	Thr	Trp	Ser	Pro	Gly	Lys	Glu	Thr	Ser	Tyr	Thr	
	50					55					60					

cag	tac	aca	gtt	aag	aga	act	tac	gct	ttt	gga	gaa	aaa	cat	gat	aat	240
Gln	Tyr	Thr	Val	Lys	Arg	Thr	Tyr	Ala	Phe	Gly	Glu	Lys	His	Asp	Asn	
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Cys	Thr	Thr	Asn	Ser	Ser	Thr	Ser	Glu	Asn	Arg	Ala	Ser	Cys	Ser	Phe	
				85					90					95		

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Phe	Leu	Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile	Glu	Val	Glu	
			100					105					110			

gct	gaa	aat	gga	gat	ggt	gta	att	aaa	tct	cat	atg	aca	tac	tgg	aga	384
Ala	Glu	Asn	Gly	Asp	Gly	Val	Ile	Lys	Ser	His	Met	Thr	Tyr	Trp	Arg	
		115					120					125				

tta	gag	aac	ata	gcg	aaa	act	gaa	cca	cct	aag	att	ttc	cgt	gtg	aaa	432
Leu	Glu	Asn	Ile	Ala	Lys	Thr	Glu	Pro	Pro	Lys	Ile	Phe	Arg	Val	Lys	
	130					135					140					

cca	gtt	ttg	ggc	atc	aaa	cga	atg	att	caa	att	gaa	tgg	ata	aag	cct	480
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Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg	
180 185 190	
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Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr	
195 200 205	
gaa tat gtc ata gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg	672
Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp	
210 215 220	
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Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro	
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Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly	
245 250 255	
aga agg cca gtg cgg ttg tta tgg aag aag gca aga gga gcc cca gtc	816
Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val	
260 265 270	
cta gag aaa aca ctt ggc tac aac ata tgg tac tat cca gaa agc aac	864
Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn	
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Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu	
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Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu	
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Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp	
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Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser	
370 375 380	
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Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys	
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Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His	
405 410 415	
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Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly	
420 425 430	
gtt cca tca gaa ggt cct gag acc aag gtg gag aac att ggc gtg aag	1344
Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys	
435 440 445	
acg gtc acg atc aca tgg aaa gag att ccc aag agt gag aga aag ggt	1392
Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly	
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Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly	
465 470 475 480	
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Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser	
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ctg aaa cga aag acc tct tac att gtt cag gtc atg gcc agc acc agt	1536

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Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	Ala	Ser	Thr	Ser		
			500					505					510				
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Ala	Gly	Gly	Thr	Asn	Gly	Thr	Ser	Ile	Asn	Phe	Lys	Thr	Leu	Ser	Phe		
			515				520					525					
agt	gtc	ttt	gag	gag	ccc	aga	tct	tca	gac	aaa	act	cac	aca	tgc	cca		1632
Ser	Val	Phe	Glu	Glu	Pro	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro		
			530				535				540						
ccg	tgc	cca	gca	cct	gaa	gcc	gag	ggg	gca	ccg	tca	gtc	ttc	ctc	ttc		1680
Pro	Cys	Pro	Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe		
					550					555					560		
ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc		1728
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val		
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aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc		1776
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe		
				580				585					590				
aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg		1824
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro		
			595				600					605					
cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc		1872
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr		
			610				615					620					
gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc		1920
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val		
					630				635						640		
tcc	aac	aaa	gcc	ctc	cca	tcc	tcc	atc	gag	aaa	acc	atc	tcc	aaa	gcc		1968
Ser	Asn	Lys	Ala	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala		
				645					650					655			
aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg		2016
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg		
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09892949 54626860

gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc 2064
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 675 680 685

ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg 2112
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 690 695 700

gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc 2160
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 705 710 715 720

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag 2208
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 725 730 735

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac 2256
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
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 35 40 45
 Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
 50 55 60

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Gln	Tyr	Thr	Val	Lys	Arg	Thr	Tyr	Ala	Phe	Gly	Glu	Lys	His	Asp	Asn
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Phe	Leu	Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile	Glu	Val	Glu
			100					105					110		
Ala	Glu	Asn	Gly	Asp	Gly	Val	Ile	Lys	Ser	His	Met	Thr	Tyr	Trp	Arg
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Leu	Glu	Asn	Ile	Ala	Lys	Thr	Glu	Pro	Pro	Lys	Ile	Phe	Arg	Val	Lys
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Pro	Val	Leu	Gly	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp	Ile	Lys	Pro
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Glu	Leu	Ala	Pro	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu	Arg	Phe	Arg
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Thr	Val	Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala	Lys	Asn	Arg
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Lys	Asp	Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln	Pro	Phe	Thr
	195					200						205			
Glu	Tyr	Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser	Lys	Phe	Trp
	210					215					220				
Ser	Asp	Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Glu	Ala	Pro
225				230						235					240
Cys	Gly	Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu	Ala	Asp	Gly
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Arg	Arg	Pro	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val
		260						265					270		
Leu	Glu	Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro	Glu	Ser	Asn
	275					280						285			
Thr	Asn	Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln	Leu	Glu	Leu
	290					295					300				
His	Leu	Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser	Tyr	Asn	Ser
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Leu	Gly	Lys	Ser	Pro	Val	Ala	Thr	Leu	Arg	Ile	Pro	Ala	Ile	Gln	Glu
			325						330					335	
Lys	Ser	Phe	Gln	Cys	Ile	Glu	Val	Met	Gln	Ala	Cys	Val	Ala	Glu	Asp
		340						345					350		
Gln	Leu	Val	Val	Lys	Trp	Gln	Ser	Ser	Ala	Leu	Asp	Val	Asn	Thr	Trp
	355					360						365			
Met	Ile	Glu	Trp	Phe	Pro	Asp	Val	Asp	Ser	Glu	Pro	Thr	Thr	Leu	Ser
	370					375					380				
Trp	Glu	Ser	Val	Ser	Gln	Ala	Thr	Asn	Trp	Thr	Ile	Gln	Gln	Asp	Lys
385				390						395					400

DIRECTOR GENERAL

Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His
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 Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly
 420 425 430
 Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys
 435 440 445
 Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly
 450 455 460
 Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly
 465 470 475 480
 Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser
 485 490 495
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 Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe
 515 520 525
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 Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
 545 550 555 560
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
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 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
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 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 595 600 605
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
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 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 625 630 635 640
 Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
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 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 660 665 670
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 675 680 685
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
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 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
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 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 725 730 735

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Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
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<400> 86
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<210> 87
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 Met
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 Val Gln Pro Leu Gly Val Asn Ala Gly Ile Met Trp Thr Leu Ala Leu
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 Trp Ala Phe Ser Phe Leu Cys Lys Phe Ser Leu Ala Val Leu Pro Thr
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aag cca gag aac att tcc tgc gtc ttt tac ttc gac aga aat ctg act 431
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 Cys Thr Trp Arg Pro Glu Lys Glu Thr Asn Asp Thr Ser Tyr Ile Val
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act ttg act tac tcc tat gga aaa agc aat tat agt gac aat gct aca 527
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gac atc aca tat tgg cat tta atc tcc ata gca aaa acc gaa cca cct 671

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Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro Leu	
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 Gly His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu
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 Gly Thr Pro Leu Lys Gly Pro Glu Thr Arg Val Glu Asn Ile Gly Leu
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 Arg Ala Gly Gly Thr Asn Gly Val Arg Ile Asn Phe Lys Thr Leu Ser
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 Gly Asn Val
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